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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: markspencer

Timestamp: [year=2010; month=3; day=16; hr=7; min=57; sec=39; ms=774;]

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Reviewer Comments:

1.

W402	Undefined organism found in <213> in SEQ ID (1)
E311	Invalid field content in <220> in SEQ ID (1)
E257	Invalid sequence data feature in <221> in SEQ ID (1)
W401	Unrecognized range formatin <222> in SEQID (1)
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error has occured more than 20 times, will not be displayed
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has occured more than 20 times, will not be displayed
E257 Invalid sequence data feature in <221> in SEQ ID (20)
This error has occured more than 20 times, will not be displayed
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error has occured more than 20 times, will not be displayed

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<221> NAME/KEY: Modified-base
<222> LOCATION: (1), (2), (3), (13), (14), (15)
<223> OTHER INFORMATION: beta-D-amino-LNA Monomer
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For SEQ ID # 1 through 30, please remove all subject line headers from the entire sequence listing. Example: "<213> ORGANISM: ARTIFICIAL SEQUENCE" should be "<213> ARTIFICIAL SEQUENCE". Please remove subject line headers "FEATURE", "NAME/KEY:", "LOCATION:", and "OTHER INFORMATION:" from numeric identifiers <220>, <221>, <222>, and <223> respectively. Please make all necessary changes.

For SEQ ID # 1 through 30, when using "Artificial sequence", for numeric identifier <213>, a mandatory feature is required to explain the source of the genetic material. The feature consists of numeric identifier <220>, which remains blank and numeric identifier <223>, which states the source of the genetic material. To explain the source, if the sequence is put together from several organisms, please list those organisms. If the sequence is made in the laboratory, please indicate that the sequence is synthesized. Please make all necessary changes.

Application No: 10535472 Version No: 1.0

Input Set:**Output Set:**

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Finished: 2010-03-03 18:40:29.095
Elapsed: 0 hr(s) 0 min(s) 22 sec(s) 93 ms
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Total Errors: 60
No. of SeqIDs Defined: 30
Actual SeqID Count: 30

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W 401	Unrecognized range formatin <222> in SEQID (2)
W 402	Undefined organism found in <213> in SEQ ID (3)
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E 257	Invalid sequence data feature in <221> in SEQ ID (3)
W 401	Unrecognized range formatin <222> in SEQID (3)
W 402	Undefined organism found in <213> in SEQ ID (4)
E 311	Invalid field content in <220> in SEQ ID (4)
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W 401	Unrecognized range formatin <222> in SEQID (4)
W 402	Undefined organism found in <213> in SEQ ID (5)
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Input Set:

Output Set:

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No. of SeqIDs Defined: 30
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W 402	Undefined organism found in <213> in SEQ ID (7)
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E 311	Invalid field content in <220> in SEQ ID (11)

Input Set:

Output Set:

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Error code	Error Description
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W 402	Undefined organism found in <213> in SEQ ID (15)
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Input Set:

Output Set:

Started: 2010-03-03 18:40:07.002
Finished: 2010-03-03 18:40:29.095
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Total Errors: 60
No. of SeqIDs Defined: 30
Actual SeqID Count: 30

Error code	Error Description
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E 311	Invalid field content in <220> in SEQ ID (17)
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W 402	Undefined organism found in <213> in SEQ ID (18)
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E 257	Invalid sequence data feature in <221> in SEQ ID (19)
W 401	Unrecognized range formatin <222> in SEQID (19)
W 402	Undefined organism found in <213> in SEQ ID (20) This error has occurred more than 20 times, will not be displayed
E 311	Invalid field content in <220> in SEQ ID (20) This error has occurred more than 20 times, will not be displayed
E 257	Invalid sequence data feature in <221> in SEQ ID (20) This error has occurred more than 20 times, will not be displayed
W 401	Unrecognized range formatin <222> in SEQID (20) This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> Christenson, Signe M.
 Mikkelsen, Nikolaj D.
 Frieden, Miriam
 Hansen, Henrik F.
 Koch, Troels
 Pedersen, Daniel S.
 Rosenbohm, Christoph
 Thruue, Charlotte A.
 Westergaard, Majken

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